11th GERMPLASM & BREEDING

8th MOLECULAR BIOLOGY

ISSCT WORKSHOP

Saint-Gilles Réunion Island / 1–5 June 2015



« Pushing the frontiers of sugarcane improvement »

ABSTRACT

11th GERMPLASM & BREEDING

8th MOLECULAR BIOLOGY WORKSHOP

Saint-Gilles Réunion Island / 1–5 June 2015

COMMITTEES

Scientific Commission

Chair – **Dr Phillip Jackson**
ISSCT Germplasm and Breeding Committee
CSIRO – Australia - Phillip.Jackson@csiro.au

Chair – **Dr Angélique D'Hont**
ISSCT Molecular Biology Committe
CIRAD – France - dhont@cirad.fr

Organizing committee

Audrey Thong-Chane
eRcane
thong-chane@ercane.re / Cel + 262 (0) 692 87 91 83

Laurent Barau
eRcane
barau@ercane.re / Cel + 262 (0) 692 88 68 53

Jean-Yves Hoarau
eRcane/Cirad
hoarau@ercane.re / Cel + 262 (0) 692 75 78 40

ORGANIZATION

SUMMARY

MO4

TOWARD A REFERENCE SEQUENCE OF THE SUGARCANE GENOME

Olivier Garsmeur[1], Carine Charron[1], Bernard Potier[2], Karen Aitken[3], Paul Berkman[3], Gaetan Droc[1], Guillaume Martin[1], Edwin van der Vossen[4], Robert Henry[5] and Angélique D'Hont[1].

[1] CIRAD (Centre de coopération Internationale en Recherche Agronomique pour le Développement), UMR AGAP, F-34398 Montpellier, France.
[2] SASRI (South African Sugarcane Research Institute), Mount Edgecombe, 4300, South Africa.
[3] CSIRO (Commonwealth Scientific and Industrial Research Organisation), Agriculture, St Lucia, QLD 4067, Australia.
[4] Keygene N.V., Agro Business Park 90, 6708 PW, Wageningen, the Netherlands.
[5] QAAFI (Queensland Alliance for Agriculture and Food Innovation), University of Queensland, St Lucia, QLD 4072, Australia.

E-mail: dhont@cirad.fr

Keywords: Sugarcane, genome, sequencing, reference, genes

The sugarcane genome poses challenges that have not been addressed in any prior genome sequencing project. The main difficulties reside in the high polyploidy (2n ~ 12x ~ 120), and the high level of heterozygosity of cultivars which make an assembly of the genome very challenging through classical whole genome shotgun sequencing approaches.

We develop an approach based on previous studies that demonstrated that sugarcane hom(e)ologous chromosomes share a very high level of micro-colinearity among themselves and show good micro-colinearity with sorghum. We used the Whole Genome Profiling (WGP^{TM}) technology of Keygene to analyze a set of 20,736 BACs from cultivar R570 and map them on the sorghum genome. An average of 37.2 sequence tags per BAC was generated that allowed anchoring 11,732 of the analyzed R570 BACs on the sorghum genome. A core set of 5000 BAC representing the minimum number of BAC to best cover the gene rich part of the sorghum genome was selected. This set of 5000 BAC is currently being sequenced through international collaborations. The aim is to obtain a high quality sequence for each BAC, which mean an assembly in one or very few contigs. So far, half of the 5000 BAC have been sequenced. A sugarcane web portal is currently being developed together with friendly tools to make BAC sequences and gene annotations available through an exploitable form to the sugarcane community.

These 5000 BAC sequences will correspond to the gene rich part of the sugarcane genome and will represent a very important resource for genetic, structural and functional genomic studies in sugarcane. This high quality frame will be essential to build a whole genome sugarcane sequence when improved sequencing and assembling methods are available.
We acknowledge the International Consortium for Sugarcane Biotechnology (ICSB) members for their support.